



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/798,579
Source: INVO
Date Processed by STIC: 3/22/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses.

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313 1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/798,579

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☒ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
 (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
 (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 ☐ Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 0001/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/798,579

DATE: 03/22/2004
TIME: 10:19:03

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\03222004\J798579.raw

2 <110> APPLICANT: Kirin Beer Kabushiki Kaisha; Japan International Research Center f
3 or Agricultural Sciences
5 <120> TITLE OF INVENTION: A production of plants having improved rooting efficiency
and vase

6 life by using environmental stress-resistant gene

8 <130> FILE REFERENCE: PH-2034

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/798,579

C--> 10 <141> CURRENT FILING DATE: 2004-03-12

10 <150> PRIOR APPLICATION NUMBER: JP 2003-071082

11 <151> PRIOR FILING DATE: 2003-03-14

13 <160> NUMBER OF SEQ ID NOS: 30

ERRORED SEQUENCES

73 <210> SEQ ID NO: 2
74 <211> LENGTH: 216
75 <212> TYPE: PRT
76 <213> ORGANISM: Arabidopsis thaliana
78 <400> SEQUENCE: 2
79 Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu
E--> 80 1 5 10 15 20
81 Ser Ser Val Ser Ser Gly Gly Asp Tyr Ile Pro Thr Leu Ala Ser Ser
E--> 82 25 30 35 40 45
83 Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His
E--> 84 50 55 60 65 70
85 Pro Ile Tyr Arg Gly Val Arg Arg Asn Ser Gly Lys Trp Val Cys
E--> 86 75 80 85 90 95
87 Glu Val Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe
E--> 88 65 70 75 80 85
89 Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala
E--> 90 95 100 105 110 115
91 Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg
E--> 92 120 125 130 135 140
93 Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala
E--> 94 145 150 155 160 165
95 Ala Glu Ala Ala Leu Ala Phe Gln Asp Glu Met Cys Asp Ala Thr Thr
E--> 96 170 175 180 185 190
97 Asp His Gly Phe Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr Thr
E--> 98 195 200 205 210 215
99 Ala Glu Gln Ser Glu Asn Ala Phe Tyr Met His Asp Glu Ala Met Phe
E--> 100 220 225 230 235 240
101 Glu Met Pro Ser Leu Leu Ala Asn Met Ala Glu Gly Met Leu Leu Pro
E--> 102 245 250 255 260 265

PLEASE see item
3 & 4
ON error
summary sheet.
Does Not Comply
Corrected Diskette Needed
(PS. 1-15)

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/798,579

DATE: 03/22/2004

TIME: 10:19:03

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\03222004\J798579.raw

103 Leu Pro Ser Val Gln Trp Asn His Asn His Glu Val Asp Gly Asp Asp
E--> 104 195 200 205
105 Asp Asp Val Ser Leu Trp Ser Tyr
E--> 106 210 215
191 <210> SEQ ID NO: 4
192 <211> LENGTH: 335
193 <212> TYPE: PRT
194 <213> ORGANISM: Arabidopsis thaliana
196 <400> SEQUENCE: 4
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E--> 198 1 5 10 15
199 Thr Ser Arg Lys Arg Lys Ser Arg Ser Arg Gly Asp Gly Thr Thr Val
E--> 200 20 25 30
201 Ala Glu Arg Leu Lys Arg Trp Lys Glu Tyr Asn Glu Thr Val Glu Glu
E--> 202 35 40 45
203 Val Ser Thr Lys Lys Arg Lys Val Pro Ala Lys Gly Ser Lys Lys Gly
E--> 204 50 55 60
205 Cys Met Lys Gly Lys Gly Gly Pro Glu Asn Ser Arg Cys Ser Phe Arg
E--> 206 65 70 75 80
207 Gly Val Arg Gln Arg Ile Trp Gly Lys Trp Val Ala Glu Ile Arg Glu
E--> 208 85 90 95
209 Pro Asn Arg Gly Ser Arg Leu Trp Leu Gly Thr Phe Pro Thr Ala Gln
E--> 210 100 105 110
211 Glu Ala Ala Ser Ala Tyr Asp Glu Ala Ala Lys Ala Met Tyr Gly Pro
E--> 212 115 120 125
213 Leu Ala Arg Leu Asn Phe Pro Arg Ser Asp Ala Ser Glu Val Thr Ser
E--> 214 130 135 140
215 Thr Ser Ser Gln Ser Glu Val Cys Thr Val Glu Thr Pro Gly Cys Val
E--> 216 145 150 155 160
217 His Val Lys Thr Glu Asp Pro Asp Cys Glu Ser Lys Pro Phe Ser Gly
E--> 218 165 170 175
219 Gly Val Glu Pro Met Tyr Cys Leu Glu Asn Gly Ala Glu Glu Met Lys
E--> 220 180 185 190
221 Arg Gly Val Lys Ala Asp Lys His Trp Leu Ser Glu Phe Glu His Asn
E--> 222 195 200 205
223 Tyr Trp Ser Asp Ile Leu Lys Glu Lys Glu Lys Gln Lys Glu Gln Gly
E--> 224 210 215 220
225 Ile Val Glu Thr Cys Gln Gln Gln Gln Gln Asp Ser Leu Ser Val Ala
E--> 226 225 230 235 240
227 Asp Tyr Gly Trp Pro Asn Asp Val Asp Gln Ser His Leu Asp Ser Ser
E--> 228 245 250 255
229 Asp Met Phe Asp Val Asp Glu Leu Leu Arg Asp Leu Asn Gly Asp Asp
E--> 230 260 265 270
231 Val Phe Ala Gly Leu Asn Gln Asp Arg Tyr Pro Gly Asn Ser Val Ala
E--> 232 275 280 285
233 Asn Gly Ser Tyr Arg Pro Glu Ser Gln Gln Ser Gly Phe Asp Pro Leu
E--> 234 290 295 300
235 Gln Ser Leu Asn Tyr Gly Ile Pro Pro Phe Gln Leu Glu Gly Lys Asp
E--> 236 305 310 315 320

same errors
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Input Set : A:\PTO.DA.txt

Output Set : N:\CRF4\03222004\J798579.raw

237 Gly Asn Gly Phe Phe Asp Asp Leu Ser Tyr Leu Asp Leu Glu Asn
 E--> 238 325 330 335
 300 <210> SEQ ID NO: 6
 301 <211> LENGTH: 213
 302 <212> TYPE: PRT
 303 <213> ORGANISM: Arabidopsis thaliana
 305 <400> SEQUENCE: 6
 306 Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu
 E--> 307 1 5 10 15
 308 Pro Gln Gly Gly Asp Tyr Cys Pro Thr Leu Ala Thr Ser Cys Pro Lys
 E--> 309 20 25 30
 310 Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His Pro Ile Tyr
 E--> 311 35 40 45
 312 Arg Gly Val Arg Gln Arg Asn Ser Gly Lys Trp Val Ser Glu Val Arg
 E--> 313 50 55 60
 314 Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala
 E--> 315 65 70 75 80
 316 Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala Leu Arg Gly
 E--> 317 85 90 95
 318 Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile
 E--> 319 100 105 110
 320 Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala Ala Glu Ala
 E--> 321 115 120 125
 322 Ala Leu Ala Phe Gln Asp Glu Thr Cys Asp Thr Thr Thr Asn His
 E--> 323 130 135 140
 324 Gly Leu Asp Met Glu Glu Thr Met Val Glu Ala Ile Tyr Thr Pro Glu
 E--> 325 145 150 155 160
 326 Gln Ser Glu Gly Ala Phe Tyr Met Asp Glu Glu Thr Met Phe Gly Met
 E--> 327 165 170 175
 328 Pro Thr Leu Leu Asp Asn Met Ala Glu Gly Met Leu Leu Pro Pro Pro
 E--> 329 180 185 190
 330 Ser Val Gln Trp Asn His Asn Tyr Asp Gly Glu Gly Asp Gly Asp Val
 E--> 331 195 200 205
 332 Ser Leu Trp Ser Tyr
 E--> 333 210
 393 <210> SEQ ID NO: 8
 394 <211> LENGTH: 216
 395 <212> TYPE: PRT
 396 <213> ORGANISM: Arabidopsis thaliana
 398 <400> SEQUENCE: 8
 399 Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu
 E--> 400 1 5 10 15
 401 Ser Pro Val Ser Ser Gly Gly Asp Tyr Ser Pro Lys Leu Ala Thr Ser
 E--> 402 20 25 30
 403 Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His
 E--> 404 35 40 45
 405 Pro Ile Tyr Arg Gly Val Arg Gln Arg Asn Ser Gly Lys Trp Val Cys
 E--> 406 50 55 60
 407 Glu Leu Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe

Same
 errors

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Input Set : A:\PTO.DA.txt
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E--> 408 65 70 75 80
409 Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Ile Ala
E--> 410 85 90 95
411 Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg
E--> 412 100 105 110
413 Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Glu Ile Gln Lys Ala Ala
E--> 414 115 120 125
415 Ala Glu Ala Ala Leu Asn Phe Gln Asp Glu Met Cys His Met Thr Thr
E--> 416 130 135 140
417 Asp Ala His Gly Leu Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr
E--> 418 145 150 155 160
419 Thr Pro Glu Gln Ser Gln Asp Ala Phe Tyr Met Asp Glu Glu Ala Met
E--> 420 165 170 175
421 Leu Gly Met Ser Ser Leu Leu Asp Asn Met Ala Glu Gly Met Leu Leu
E--> 422 180 185 190
423 Pro Ser Pro Ser Val Gln Trp Asn Tyr Asn Phe Asp Val Glu Gly Asp
E--> 424 195 200 205
425 Asp Asp Val Ser Leu Trp Ser Tyr
E--> 426 210 215
517 <210> SEQ ID NO: 10
518 <211> LENGTH: 330
519 <212> TYPE: PRT
520 <213> ORGANISM: Arabidopsis thaliana
W--> 521 <400> SEQUENCE: 10
522 Met Ala Val Tyr Glu Gln Thr Gly Thr Glu Gln Pro Lys Lys Arg Lys
E--> 523 1 5 10 15
524 Ser Arg Ala Arg Ala Gly Gly Leu Thr Val Ala Asp Arg Leu Lys Lys
E--> 525 20 25 30
526 Trp Lys Glu Tyr Asn Glu Ile Val Glu Ala Ser Ala Val Lys Glu Gly
E--> 527 35 40 45
528 Glu Lys Pro Lys Arg Lys Val Pro Ala Lys Gly Ser Lys Lys Gly Cys
E--> 529 50 55 60
530 Met Lys Gly Lys Gly Gly Pro Asp Asn Ser His Cys Ser Phe Arg Gly
E--> 531 65 70 75 80
532 Val Arg Gln Arg Ile Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro
E--> 533 85 90 95
534 Lys Ile Gly Thr Arg Leu Trp Leu Gly Thr Phe Pro Thr Ala Glu Lys
E--> 535 100 105 110
536 Ala Ala Ser Ala Tyr Asp Glu Ala Ala Thr Ala Met Tyr Gly Ser Leu
E--> 537 115 120 125
538 Ala Arg Leu Asn Phe Pro Gln Ser Val Gly Ser Glu Phe Thr Ser Thr
E--> 539 130 135 140
540 Ser Ser Gln Ser Glu Val Cys Thr Val Glu Asn Lys Ala Val Val Cys
E--> 541 145 150 155 160
542 Gly Asp Val Cys Val Lys His Glu Asp Thr Asp Cys Glu Ser Asn Pro
E--> 543 165 170 175
544 Phe Ser Gln Ile Leu Asp Val Arg Glu Glu Ser Cys Gly Thr Arg Pro
E--> 545 180 185 190
546 Asp Ser Cys Thr Val Gly His Gln Asp Met Asn Ser Ser Leu Asn Tyr

Some errors
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Input Set : A:\PTO.DA.txt

Output Set : N:\CRF4\03222004\J798579.raw

E--> 547 195 200 205
548 Asp Leu Leu Leu Glu Phe Glu Gln Gln Tyr Trp Gly Gln Val Leu Gln
E--> 549 210 215 220
550 Glu Lys Glu Lys Pro Lys Gln Glu Glu Glu Ile Gln Gln Gln Gln
E--> 551 225 230 235 240
552 Gln Glu Gln Gln Gln Gln Leu Gln Pro Asp Leu Leu Thr Val Ala
E--> 553 245 250 255
554 Asp Tyr Gly Trp Pro Trp Ser Asn Asp Ile Val Asn Asp Gln Thr Ser
E--> 555 260 265 270
556 Trp Asp Pro Asn Glu Cys Phe Asp Ile Asn Glu Leu Leu Gly Asp Leu
E--> 557 275 280 285
558 Asn Glu Pro Gly Pro His Gln Ser Gln Asp Gln Asn His Val Asn Ser
E--> 559 290 295 300
560 Gly Ser Tyr Asp Leu His Pro Leu His Leu Glu Pro His Asp Gly His
E--> 561 305 310 315 320
562 Glu Phe Asn Gly Leu Ser Ser Leu Asp Ile
E--> 563 325 330
584 <210> SEQ ID NO: 12
585 <211> LENGTH: 224
586 <212> TYPE: PRT
587 <213> ORGANISM: Arabidopsis thaliana
589 <400> SEQUENCE: 12
590 Met Asn Pro Phe Tyr Ser Thr Phe Pro Asp Ser Phe Leu Ser Ile Ser
E--> 591 1 5 10 15
593 Asp His Arg Ser Pro Val Ser Asp Ser Ser Glu Cys Ser Pro Lys Leu
E--> 594 20 25 30
596 Ala Ser Ser Cys Pro Lys Lys Arg Ala Gly Arg Lys Lys Phe Arg Glu
E--> 597 35 40 45
599 Thr Arg His Pro Ile Tyr Arg Gly Val Arg Gln Arg Asn Ser Gly Lys
E--> 600 50 55 60
602 Trp Val Cys Glu Val Arg Glu Pro Asn Lys Lys Ser Arg Ile Trp Leu
E--> 603 65 70 75 80
605 Gly Thr Phe Pro Thr Val Glu Met Ala Ala Arg Ala His Asp Val Ala
E--> 606 85 90 95
608 Ala Leu Ala Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser
E--> 609 100 105 110
611 Ala Trp Arg Leu Arg Ile Pro Glu Thr Thr Cys Pro Lys Glu Ile Gln
E--> 612 115 120 125
614 Lys Ala Ala Ser Glu Ala Ala Met Ala Phe Gln Asn Glu Thr Thr Thr
E--> 615 130 135 140
617 Glu Gly Ser Lys Thr Ala Ala Glu Ala Glu Glu Ala Ala Gly Glu Gly
E--> 618 145 150 155 160
620 Val Arg Glu Gly Glu Arg Arg Ala Glu Glu Gln Asn Gly Gly Val Phe
E--> 621 165 170 175
623 Tyr Met Asp Asp Glu Ala Leu Leu Gly Met Pro Asn Phe Phe Glu Asn
E--> 624 180 185 190
626 Met Ala Glu Gly Met Leu Leu Pro Pro Pro Glu Val Gly Trp Asn His
E--> 627 195 200 205
629 Asn Asp Phe Asp Gly Val Gly Asp Val Ser Leu Trp Ser Phe Asp Glu

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E--> 630 210 215 220
650 <210> SEQ ID NO: 14
651 <211> LENGTH: 181
652 <212> TYPE: PRT
653 <213> ORGANISM: Arabidopsis thaliana
655 <400> SEQUENCE: 14
656 Met Glu Asn Asp Asp Ile Thr Val Ala Glu Met Lys Pro Lys Lys Arg
E--> 657 1 5 10 15
659 Ala Gly Arg Arg Ile Phe Lys Glu Thr Arg His Pro Ile Tyr Arg Gly
E--> 660 20 25 30
662 Val Arg Arg Arg Asp Gly Asp Lys Trp Val Cys Glu Val Arg Glu Pro
E--> 663 35 40 45
665 Ile His Gln Arg Arg Val Trp Leu Gly Thr Tyr Pro Thr Ala Asp Met
E--> 666 50 55 60
668 Ala Ala Arg Ala His Asp Val Ala Val Leu Ala Leu Arg Gly Arg Ser
E--> 669 65 70 75 80
671 Ala Cys Leu Asn Phe Ser Asp Ser Ala Trp Arg Leu Pro Val Pro Ala
E--> 672 85 90 95
674 Ser Thr Asp Pro Asp Thr Ile Arg Arg Thr Ala Ala Glu Ala Ala Glu
E--> 675 100 105 110
677 Met Phe Arg Pro Pro Glu Phe Ser Thr Gly Ile Thr Val Leu Pro Ser
E--> 678 115 120 125
680 Ala Ser Glu Phe Asp Thr Ser Asp Glu Gly Val Ala Gly Met Met Met
E--> 681 130 135 140
683 Arg Leu Ala Glu Glu Pro Leu Met Ser Pro Pro Arg Ser Tyr Ile Asp
E--> 684 145 150 155 160
686 Met Asn Thr Ser Val Tyr Val Asp Glu Glu Met Cys Tyr Glu Asp Leu
E--> 687 165 170 175
689 Ser Leu Trp Ser Tyr
E--> 690 180
709 <210> SEQ ID NO: 16
710 <211> LENGTH: 209
711 <212> TYPE: PRT
712 <213> ORGANISM: Arabidopsis thaliana
714 <400> SEQUENCE: 16
715 Met Asn Asn Asp Asp Ile Ile Leu Ala Glu Met Arg Pro Lys Lys Arg
E--> 716 1 5 10 15
717 Ala Gly Arg Arg Val Phe Lys Glu Thr Arg His Pro Val Tyr Arg Gly
E--> 718 20 25 30
720 Ile Arg Arg Arg Asn Gly Asp Lys Trp Val Cys Glu Val Arg Glu Pro
E--> 721 35 40 45
723 Thr His Gln Arg Arg Ile Trp Leu Gly Thr Tyr Pro Thr Ala Asp Met
E--> 724 50 55 60
726 Ala Ala Arg Ala His Asp Val Ala Val Leu Ala Leu Arg Gly Arg Ser
E--> 727 65 70 75 80
729 Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg Leu Pro Val Pro Glu
E--> 730 85 90 95
732 Ser Asn Asp Pro Asp Val Ile Arg Arg Val Ala Ala Glu Ala Ala Glu
E--> 733 100 105 110

Same errors

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Input Set : A:\PTO.DA.txt
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735 Met Phe Arg Pro Val Asp Leu Glu Ser Gly Ile Thr Val Leu Pro Cys
E--> 736 115 120 125
738 Ala Gly Asp Asp Val Asp Leu Gly Phe Gly Ser Gly Ser Gly Ser Gly
E--> 739 130 135 140
741 Ser Gly Ser Glu Glu Arg Asn Ser Ser Ser Tyr Gly Phe Gly Asp Tyr
E--> 742 145 150 155 160
744 Glu Glu Val Ser Thr Thr Met Met Arg Leu Ala Glu Gly Pro Leu Met
E--> 745 165 170 175
746 Ser Pro Pro Arg Ser Tyr Met Glu Asp Met Thr Pro Thr Asn Val Tyr
E--> 747 180 185 190
749 Thr Glu Glu Glu Met Cys Tyr Glu Asp Met Ser Leu Trp Ser Tyr Arg
E--> 750 195 200 205
752 Tyr
781 <210> SEQ ID NO: 18
782 <211> LENGTH: 341
783 <212> TYPE: PRT
784 <213> ORGANISM: Arabidopsis thaliana
786 <400> SEQUENCE: 18
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E--> 788 1 5 10 15
790 Asp Val Ala Glu Ile Leu Arg Gln Trp Arg Glu Tyr Asn Glu Gln Ile
E--> 791 20 25 30
793 Glu Ala Glu Ser Cys Ile Asp Gly Gly Gly Pro Lys Ser Ile Arg Lys
E--> 794 35 40 45
796 Pro Pro Pro Lys Gly Ser Arg Lys Gly Cys Met Lys Gly Lys Gly Gly
E--> 797 50 55 60
799 Pro Glu Asn Gly Ile Cys Asp Tyr Arg Gly Val Arg Gln Arg Arg Trp
E--> 800 65 70 75 80
801 Gly Lys Trp Val Ala Glu Ile Arg Glu Pro Asp Gly Gly Ala Arg Leu
E--> 802 85 90 95
804 Trp Leu Gly Thr Phe Ser Ser Ser Tyr Glu Ala Ala Leu Ala Tyr Asp
E--> 805 100 105 110
807 Glu Ala Ala Lys Ala Ile Tyr Gly Gln Ser Ala Arg Leu Asn Leu Pro
E--> 808 115 120 125
810 Glu Ile Thr Asn Arg Ser Ser Ser Thr Ala Ala Thr Ala Thr Val Ser
E--> 811 130 135 140
813 Gly Ser Val Thr Ala Phe Ser Asp Glu Ser Glu Val Cys Ala Arg Glu
E--> 814 145 150 155 160
816 Asp Thr Asn Ala Ser Ser Gly Phe Gly Gln Val Lys Leu Glu Asp Cys
E--> 817 165 170 175
819 Ser Asp Glu Tyr Val Leu Leu Asp Ser Ser Gln Cys Ile Lys Glu Glu
E--> 820 180 185 190
822 Leu Lys Gly Lys Glu Glu Val Arg Glu Glu His Asn Leu Ala Val Gly
E--> 823 195 200 205
825 Phe Gly Ile Gly Gln Asp Ser Lys Arg Glu Thr Leu Asp Ala Trp Leu
E--> 826 210 215 220
828 Met Gly Asn Gly Asn Glu Gln Glu Pro Leu Glu Phe Gly Val Asp Glu
E--> 829 225 230 235 240
830 Thr Phe Asp Ile Asn Glu Leu Leu Gly Ile Leu Asn Asp Asn Asn Val

← Same errors

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E--> 831 245 250 255
833 Ser Gly Gln Glu Thr Met Gln Tyr Gln Val Asp Arg His Pro Asn Phe
E--> 834 260 265 270
836 Ser Tyr Gln Thr Gln Phe Pro Asn Ser Asn Leu Leu Gly Ser Leu Asn
E--> 837 275 280 285
839 Pro Met Glu Ile Ala Gln Pro Gly Val Asp Tyr Gly Cys Pro Tyr Val
E--> 840 290 295 300
842 Gln Pro Ser Asp Met Glu Asn Tyr Gly Ile Asp Leu Asp His Arg Arg
E--> 843 305 310 315 320
845 Phe Asn Asp Leu Asp Ile Gln Asp Leu Asp Phe Gly Gly Asp Lys Asp
E--> 846 325 330 335
848 Val His Gly Ser Thr
E--> 849 340
870 <210> SEQ ID NO: 20
871 <211> LENGTH: 206
872 <212> TYPE: PRT
873 <213> ORGANISM: Arabidopsis thaliana
875 <400> SEQUENCE: 20
876 Met Ser Ser Ile Glu Pro Lys Val Met Met Val Gly Ala Asn Lys Lys
E--> 877 1 5 10 15
879 Gln Arg Thr Val Gln Ala Ser Ser Arg Lys Gly Cys Met Arg Gly Lys
E--> 880 20 25 30
882 Gly Gly Pro Asp Asn Ala Ser Cys Thr Tyr Lys Gly Val Arg Gln Arg
E--> 883 35 40 45
885 Thr Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro Asn Arg Gly Ala
E--> 886 50 55 60
888 Arg Leu Trp Leu Gly Thr Phe Asp Thr Ser Arg Glu Ala Ala Leu Ala
E--> 889 65 70 75 80
891 Tyr Asp Ser Ala Ala Arg Lys Leu Tyr Gly Pro Glu Ala His Leu Asn
E--> 892 85 90 95
894 Leu Pro Glu Ser Leu Arg Ser Tyr Pro Lys Thr Ala Ser Ser Pro Ala
E--> 895 100 105 110
897 Ser Gln Thr Thr Pro Ser Ser Asn Thr Gly Gly Lys Ser Ser Ser Asp
E--> 898 115 120 125
900 Ser Glu Ser Pro Cys Ser Ser Asn Glu Met Ser Ser Cys Gly Arg Val
E--> 901 130 135 140
903 Thr Glu Glu Ile Ser Trp Glu His Ile Asn Val Asp Leu Pro Val Met
E--> 904 145 150 155 160
906 Asp Asp Ser Ser Ile Trp Glu Glu Ala Thr Met Ser Leu Gly Phe Pro
E--> 907 165 170 175
909 Trp Val His Glu Gly Asp Asn Asp Ile Ser Arg Phe Asp Thr Cys Ile
E--> 910 180 185 190
912 Ser Gly Gly Tyr Ser Asn Trp Asp Ser Phe His Ser Pro Leu
E--> 913 195 200 205
938 <210> SEQ ID NO: 22
939 <211> LENGTH: 244
940 <212> TYPE: PRT
941 <213> ORGANISM: Arabidopsis thaliana
943 <400> SEQUENCE: 22

same errors

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PATENT APPLICATION: US/10/798,579

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TIME: 10:19:03

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\03222004\J798579.raw

944 Met Glu Lys Glu Asp Asn Gly Ser Lys Gln Ser Ser Ser Ala Ser Val
E--> 945 1 5 10 15
947 Val Ser Ser Arg Arg Arg Arg Val Val Glu Pro Val Glu Ala Thr
E--> 948 20 25 30
950 Leu Gln Arg Trp Glu Glu Gly Leu Ala Arg Ala Arg Arg Val Gln
E--> 951 35 40 45
953 Ala Lys Gly Ser Lys Lys Gly Cys Met Arg Gly Lys Gly Gly Pro Glu
E--> 954 50 55 60
956 Asn Pro Val Cys Arg Phe Arg Gly Val Arg Gln Arg Val Trp Gly Lys
E--> 957 65 70 75 80
959 Trp Val Ala Glu Ile Arg Glu Pro Val Ser His Arg Gly Ala Asn Ser
E--> 960 85 90 95
962 Ser Arg Ser Lys Arg Leu Trp Leu Gly Thr Phe Ala Thr Ala Ala Glu
E--> 963 100 105 110
965 Ala Ala Leu Ala Tyr Asp Arg Ala Ala Ser Val Met Tyr Gly Pro Tyr
E--> 966 115 120 125
968 Ala Arg Leu Asn Phe Pro Glu Asp Leu Gly Gly Gly Arg Lys Lys Asp
E--> 969 130 135 140
970 Glu Glu Ala Glu Ser Ser Gly Gly Tyr Trp Leu Glu Thr Asn Lys Ala
E--> 971 145 150 155 160
973 Gly Asn Gly Val Ile Glu Thr Glu Gly Gly Lys Asp Tyr Val Val Tyr
E--> 974 165 170 175
976 Asn Glu Asp Ala Ile Glu Leu Gly His Asp Lys Thr Gln Asn Pro Met
E--> 977 180 185 190
979 Thr Asp Asn Glu Ile Val Asn Pro Ala Val Lys Ser Glu Glu Gly Tyr
E--> 980 195 200 205
982 Ser Tyr Asp Arg Phe Lys Leu Asp Asn Gly Leu Leu Tyr Asn Glu Pro
E--> 983 210 215 220
985 Gln Ser Ser Ser Tyr His Gln Gly Gly Gly Phe Asp Ser Tyr Phe Glu
E--> 986 225 230 235 240
988 Tyr Phe Arg Phe
1013 <210> SEQ ID NO: 24
1014 <211> LENGTH: 277
1015 <212> TYPE: PRT
1016 <213> ORGANISM: Arabidopsis thaliana
1018 <400> SEQUENCE: 24
1019 Met Glu Lys Ser Ser Ser Met Lys Gln Trp Lys Lys Gly Pro Ala Arg
E--> 1020 1 5 10 15
1022 Gly Lys Gly Gly Pro Gln Asn Ala Leu Cys Gln Tyr Arg Gly Val Arg
E--> 1023 20 25 30
1025 Gln Arg Thr Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro Lys Lys
E--> 1026 35 40 45
1028 Arg Ala Arg Leu Trp Leu Gly Ser Phe Ala Thr Ala Glu Glu Ala Ala
E--> 1029 50 55 60
1031 Met Ala Tyr Asp Glu Ala Ala Leu Lys Leu Tyr Gly His Asp Ala Tyr
E--> 1032 65 70 75 80
1034 Leu Asn Leu Pro His Leu Gln Arg Asn Thr Arg Pro Ser Leu Ser Asn
E--> 1035 85 90 95
1037 Ser Gln Arg Phe Lys Trp Val Pro Ser Arg Lys Phe Ile Ser Met Phe

Same errors

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/798,579

DATE: 03/22/2004

TIME: 10:19:03

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\03222004\J798579.raw

E--> 1038 100 105 110
1040 Pro Ser Cys Gly Met Leu Asn Val Asn Ala Gln Pro Ser Val His Ile
E--> 1041 115 120 125
1043 Ile Gln Gln Arg Leu Glu Glu Leu Lys Lys Thr Gly Leu Leu Ser Gln
E--> 1044 130 135 140
1046 Ser Tyr Ser Ser Ser Ser Ser Thr Glu Ser Lys Thr Asn Thr Ser
E--> 1047 145 150 155 160
1049 Phe Leu Asp Glu Lys Thr Ser Lys Gly Glu Thr Asp Asn Met Phe Glu
E--> 1050 165 170 175
1052 Gly Gly Asp Gln Lys Lys Pro Glu Ile Asp Leu Thr Glu Phe Leu Gln
E--> 1053 180 185 190
1054 Gln Leu Gly Ile Leu Lys Asp Glu Asn Glu Ala Glu Pro Ser Glu Val
E--> 1055 195 200 205
1057 Ala Glu Cys His Ser Pro Pro Pro Trp Asn Glu Gln Glu Glu Thr Gly
E--> 1058 210 215 220
1060 Ser Pro Phe Arg Thr Glu Asn Phe Ser Trp Asp Thr Leu Ile Glu Met
E--> 1061 225 230 235 240
1063 Pro Arg Ser Glu Thr Thr Thr Met Gln Phe Asp Ser Ser Asn Phe Gly
E--> 1064 245 250 255
1066 Ser Tyr Asp Phe Glu Asp Asp Val Ser Phe Pro Ser Ile Trp Asp Tyr
E--> 1067 260 265 270
1069 Tyr Gly Ser Leu Asp
E--> 1070 275
1096 <210> SEQ ID NO: 26
1097 <211> LENGTH: 306
1098 <212> TYPE: PRT
1099 <213> ORGANISM: Arabidopsis thaliana
1101 <400> SEQUENCE: 26
1102 Glu Glu Glu Gln Pro Pro Ala Lys Lys Arg Asn Met Gly Arg Ser Arg
E--> 1103 1 5 10 15
1105 Lys Gly Cys Met Lys Gly Lys Gly Gly Pro Glu Asn Ala Thr Cys Thr
E--> 1106 20 25 30
1108 Phe Arg Gly Val Arg Gln Arg Thr Trp Gly Lys Trp Val Ala Glu Ile
E--> 1109 35 40 45
1110 Arg Glu Pro Asn Arg Gly Thr Arg Leu Trp Leu Gly Thr Phe Asn Thr
E--> 1111 50 55 60
1113 Ser Val Glu Ala Ala Met Ala Tyr Asp Glu Ala Ala Lys Lys Leu Tyr
E--> 1114 65 70 75 80
1116 Gly His Glu Ala Lys Leu Asn Leu Val His Pro Gln Gln Gln Gln Gln
E--> 1117 85 90 95
1119 Val Val Val Asn Arg Asn Leu Ser Phe Ser Gly His Gly Ser Gly Ser
E--> 1120 100 105 110
1122 Trp Ala Tyr Asn Lys Lys Leu Asp Met Val His Gly Leu Asp Leu Gly
E--> 1123 115 120 125
1125 Leu Gly Gln Ala Ser Cys Ser Arg Gly Ser Cys Ser Glu Arg Ser Ser
E--> 1126 130 135 140
1128 Phe Leu Gln Glu Asp Asp Asp His Ser His Asn Arg Cys Ser Ser Ser
E--> 1129 145 150 155 160
1131 Ser Gly Ser Asn Leu Cys Trp Leu Leu Pro Lys Gln Ser Asp Ser Gln

same errors

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/798,579

DATE: 03/22/2004

TIME: 10:19:03

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\03222004\J798579.raw

E--> 1132 165 170 175
1134 Asp Gln Glu Thr Val Asn Ala Thr Thr Ser Tyr Gly Gly Glu Gly Gly
E--> 1135 180 185 190
1137 Gly Gly Ser Thr Leu Thr Phe Ser Thr Asn Leu Lys Pro Lys Asn Leu
E--> 1138 195 200 205
1139 Met Ser Gln Asn Tyr Gly Leu Tyr Asn Gly Ala Trp Ser Arg Phe Leu
E--> 1140 210 215 220
1142 Val Gly Gln Glu Lys Lys Thr Glu His Asp Val Ser Ser Ser Cys Gly
E--> 1143 225 230 235 240
1145 Ser Ser Asp Asn Lys Glu Ser Met Leu Val Pro Ser Cys Gly Gly Glu
E--> 1146 245 250 255
1148 Arg Met His Arg Pro Glu Leu Glu Glu Arg Thr Gly Tyr Leu Glu Met
E--> 1149 260 265 270
1151 Asp Asp Leu Leu Glu Ile Asp Asp Leu Gly Leu Leu Ile Gly Lys Asn
E--> 1152 275 280 285
1154 Gly Asp Phe Lys Asn Trp Cys Cys Glu Glu Phe Gln His Pro Trp Asn
E--> 1155 290 295 300
1157 Trp Phe
1158 305
1177 <210> SEQ ID NO: 28
1178 <211> LENGTH: 177
1179 <212> TYPE: PRT
1180 <213> ORGANISM: Arabidopsis thaliana
1182 <400> SEQUENCE: 28
1183 Met Pro Arg Lys Arg Lys Ser Arg Gly Thr Arg Asp Val Ala Glu Ile
E--> 1184 1 5 10 15
1186 Leu Arg Lys Trp Arg Glu Tyr Asn Glu Gln Thr Glu Ala Asp Ser Cys
E--> 1187 20 25 30
1189 Ile Asp Gly Gly Gly Ser Lys Pro Ile Arg Lys Ala Pro Pro Lys Arg
E--> 1190 35 40 45
1192 Ser Arg Lys Gly Cys Met Lys Gly Lys Gly Gly Pro Glu Asn Gly Ile
E--> 1193 50 55 60
1194 Cys Asp Tyr Thr Gly Val Arg Gln Arg Thr Trp Gly Lys Trp Val Ala
E--> 1195 65 70 75 80
1197 Glu Ile Arg Glu Pro Gly Arg Gly Ala Lys Leu Trp Leu Gly Thr Phe
E--> 1198 85 90 95
1200 Ser Ser Ser Tyr Glu Ala Ala Leu Ala Tyr Asp Glu Ala Ser Lys Ala
E--> 1201 100 105 110
1203 Ile Tyr Gly Gln Ser Ala Arg Leu Asn Leu Pro Leu Leu Pro Leu Cys
E--> 1204 115 120 125
1206 Gln Ala Arg Leu Leu His Phe Leu Met Asn Leu Lys Phe Val His Val
E--> 1207 130 135 140
1209 Arg Ile Gln Met Gln Asp Leu Val Leu Val Arg Ser Leu Thr Ser Arg
E--> 1210 145 150 155 160
1212 Ile Ser Lys Met Leu Ser Pro Ile Thr Ala Leu Val Lys Leu Gly Arg
E--> 1213 165 170 175
1215 Tyr
1228 <210> SEQ ID NO: 30
1229 <211> LENGTH: 18

← Same
errors

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/798,579

DATE: 03/22/2004

TIME: 10:19:03

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\03222004\J798579.raw

1230 <212> TYPE: DNA

1231 <213> ORGANISM: Artificial Sequence

1233 <220> FEATURE:

1234 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer

1236 <400> SEQUENCE: 30

1237 cgatacgtcg tcatcatc

18

E--> 1240

2/1

E--> 1241

1/9

delete

<400> 1
 cctgaactag aacagaaaga gagagaaact attatttcag caaaccatac caacaaaaaa 60
 gacagagatc ttttagttac cttatccagt ttcttgaaac agagtactct tctgatca 118
 atg aac tca ttt tct gct ttt tct gaa atg ttt ggc tcc gat tac gag 166
 Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu
 1 5 10 15
 tct tcg gtt tcc tca ggc ggt gat tat att ccg acg ctt gcg agc agc 214
 Ser Ser Val Ser Ser Gly Gly Asp Tyr Ile Pro Thr Leu Ala Ser Ser
 20 25 30

^ SAME error
 Please see
 item # 3 &
 4 on
 =
 error
 Summary
 sheet.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/798,579

DATE: 03/22/2004

TIME: 10:19:04

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\03222004\J798579.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:29 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:32 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:35 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:38 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:41 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:47 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:53 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:59 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:62 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:65 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:68 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:80 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2 ✓
M:332 Repeated in SeqNo=2
L:116 M:283 W: Missing Blank Line separator, <400> field identifier
L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 ✓
L:127 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:130 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:145 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:148 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:157 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:160 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:163 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:169 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:172 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:184 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:198 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:258 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5 ✓
L:261 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:264 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:267 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:273 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/798,579

DATE: 03/22/2004

TIME: 10:19:04

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\03222004\J798579.raw

L:276 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5 ✓
L:279 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:282 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:285 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:288 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:291 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:294 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5 ✓
L:307 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6 ✓
M:332 Repeated in SeqNo=6
L:349 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7 ✓
L:352 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7 ✓
L:400 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8 ✓
M:332 Repeated in SeqNo=8
L:514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:1432 ✓
M:341 Repeated in SeqNo=9
L:521 M:283 W: Missing Blank Line separator, <400> field identifier
L:523 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:591 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
M:332 Repeated in SeqNo=12
L:657 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
M:332 Repeated in SeqNo=14
L:716 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
M:332 Repeated in SeqNo=16
L:788 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:18
M:332 Repeated in SeqNo=18
L:877 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:20
M:332 Repeated in SeqNo=20
L:945 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
M:332 Repeated in SeqNo=22
L:1020 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:24
M:332 Repeated in SeqNo=24
L:1103 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:26
M:332 Repeated in SeqNo=26
L:1184 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:28
M:332 Repeated in SeqNo=28
L:1222 M:283 W: Missing Blank Line separator, <220> field identifier ✓
L:1240 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:19 SEQ:30
L:1240 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2 ✓
M:254 Repeated in SeqNo=30
L:1241 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2 ✓
L:1241 M:252 E: No. of Seq. differs, <211> LENGTH:Input:18 Found:20 SEQ:30 ✓